Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1 - 17 (cancelled)

18. (Currently amended) A method of determining the haplotype structures of two allelic variants of a chromosome or chromosomal fragment comprising two or more single nucleotide polymorphisms (SNPs) of interest, wherein said SNPs of interest comprise different alleles, said method comprising:

preferentially extracting one of said two allelic variants ~~variant~~ from an original nucleic acid sample comprising said two allelic variants of said chromosome ~~of~~ or chromosomal fragment to provide an enriched sample in which the level of the preferentially extracted allelic variant is from 2 to 30 times greater than the level of the allelic variant that is not preferentially extracted from the sample by contacting said chromosome or chromosomal fragment with an allele-specific hybridization probe that is complementary to the sequence of one allele of a heterozygous SNP site that is located within or near the target sequence to be haplotyped;

PCR amplifying the enriched sample to proportionately increase the level of the allelic variant that is preferentially extracted from the sample and the level of the allelic variant that is not preferentially extracted from the sample; and

identifying the alleles of the SNPs of interest that are present at higher levels in the amplified enriched sample and are located on the allelic variant that is preferentially extracted from the original nucleic acid sample; and

identifying the alleles of the SNPs of interest that are present at lower levels in the amplified enriched sample and are located on the allelic variant that is not preferentially extracted from the original nucleic acid sample.

19. (Original) The method of claim 18 wherein one of said allelic variants is preferentially extracted from said original nucleic acid sample by a solid phase extraction technique that

employs an allele-specific hybridization probe that that is fully complementary to a sequence of one allele of a heterozygous SNP site that is located on said chromosome or chromosomal fragment, wherein said allele specific hybridization probe is attached to a solid support or to a first binding molecule that is capable of binding to a second binding molecule that is attached to a solid support.

20. (Original) The method of claim 19 wherein said allele-specific hybridization probe is an oligonucleotide that is attached to a first binding molecule, and said solid phase extraction technique also employs a competitor oligonucleotide that hybridizes to the other allele of the heterozygous SNP site and that is not attached to the first binding molecule

21. (Original) The method of claim 18 wherein the genotypes of the chromosomes or chromosomal fragments are determined before one allelic variant of the chromosomes or chromosomal fragments is extracted from the original nucleic acid sample.

22. (Original) The method of claim 18 wherein the amount of the enriched allelic variant in the enriched nucleic acid fraction is from 3 to 10 times greater than the amount of the non-enriched allelic variant in the nucleic acid sample.

23. (cancelled)

24. (new) A method of determining the haplotype in a subject of a nucleic acid that contains two or more single nucleotide polymorphism (SNP) sites, each of which SNP sites has at least two different known alleles, the method comprising:

combining a sample from the subject under hybridizing conditions with an allele-specific hybridization probe that is complementary to the sequence of a first allele of a first selected SNP site;

isolating from the sample allelic variants of the nucleic acid that hybridize to the allele-specific hybridization probe, thereby obtaining a nucleic acid fraction that contains at least one allelic variant of the nucleic acid, and is enriched for the allelic variant having the first allele of the first selected SNP site (the enriched allelic variant) relative to a second allelic variant having

a second allele of the first selected SNP site (the non-enriched allelic variant), wherein when the non-enriched allelic variant is present, the enriched allelic variant is present in an amount that is from 1.5 to 100 times greater than the amount of the non-enriched allelic variant;

determining the identity of the alleles for at least a second SNP site on the nucleic acid and determining the relative amounts in the nucleic acid fraction of each of the allelic variants that contain the identified alleles, wherein, the allele of the second selected SNP site that is present in the nucleic acid fraction at a relatively higher level is located on the enriched allelic variant, and wherein the allele of the second selected SNP site that is present in the nucleic acid fraction at a relatively lower level is located on the non-enriched allelic variant.

25. (new) The method according to claim 24 wherein the nucleic acid fraction is combined under polymerase chain reaction amplification conditions with one or more primer sets, wherein the one or more primer sets hybridize to portions of the nucleic acid that flank at least a second selected one of the SNP sites

26. (new) The method according to claim 25 wherein the one or more primer sets do not hybridize to portions of the nucleic acid that flank the first selected SNP site.

27. (new) The method according to claim 24 wherein the subject is diploid.

28. (new) The method of claim 24 wherein the sample is a nucleic acid sample.

29. (new) The method according to claim 28, wherein the allele-specific hybridization probe is attached to a solid support or to a first binding molecule that is capable of binding to a second binding molecule that is attached to a solid support, and wherein the nucleic acid sample and the allele-specific hybridization probe are contacted under hybridization conditions that allow the allele-specific hybridization probe to preferentially hybridize with one allele of the first selected SNP site.

30. (new) The method of claim 29 wherein the allele-specific hybridization probe is attached to a first binding molecule.

31. (new) The method of claim 30 wherein the first binding molecule is biotin or streptavidin and said second binding molecule is streptavidin or biotin, respectively.

32. (new) The method of claim 24 wherein the enriched allelic variant is present in an amount that is from 2 to 30 times greater than the amount of the non-enriched allelic variant.

33. (new) The method of claim 24 wherein the nucleic acid fraction comprises nucleic acid molecules that do not hybridize to the allele-specific hybridization probe.

34. (new) The method of claim 24 wherein the allele-specific hybridization probe is an oligonucleotide, a peptide nucleic acid or a locked nucleic acid.

35. (new) The method of claim 29 wherein the allele-specific hybridization probe is an oligonucleotide that is attached to a first binding molecule and the nucleic acid sample is contacted with both the allele-specific hybridization probe and a competitor oligonucleotide that hybridizes to the other allele of the first selected SNP site and that is not attached to the first binding molecule.

36. (new) The method according to claim 24 wherein the enriched allelic variant is present in an amount that is from 3 to 6 times greater than the amount of the non-enriched allelic variant.